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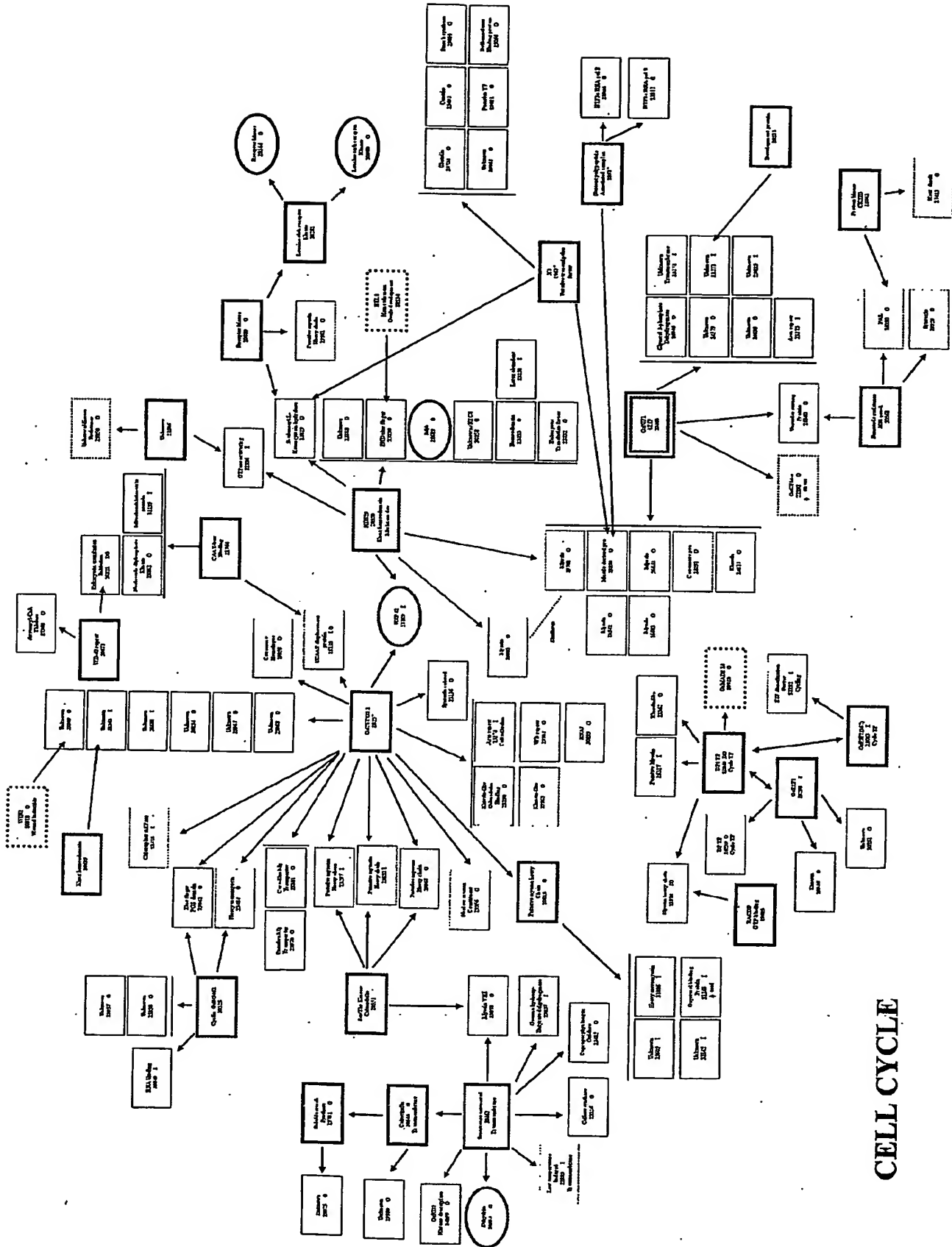


FIGURE 1C

CELL CYCLE

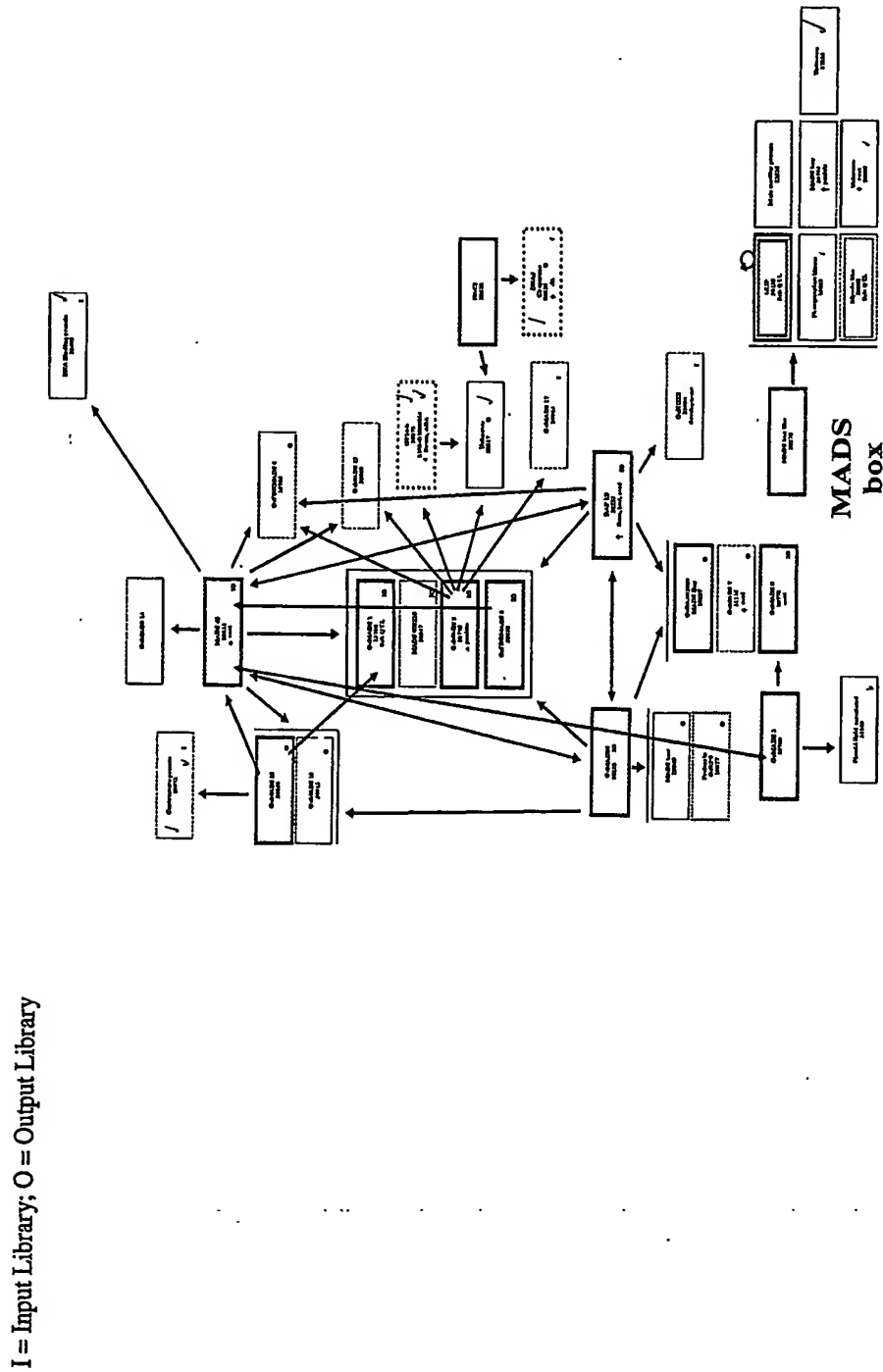


FIGURE 3A

Cons. -A-QQ-PPHSSS-F-HREAA-EPTLNIGY---AAGERIA-----Q-----LPP-WML-----
 19766 -----SSSSSSFFMMREA---LPTTNISN-YPAAAGER-----IEDVAAGQPQHVRIG-LPPWMLSHING-----
 20910 -----SSSSSSFFMMREA---LPTTNISN-YPAAAGER-----IEDVAAGQPQHERIG-LPPWMLSHING-----
 20232 -----ISSSSSFFMMREA---LPTTNISN-YPAAAGER-----IEDVPAGQPQHVRIG-LPPWMLSHING-----
 20842 QAQAQPOAQTSSTSSSSMLRDQQAALLPPQNICY-PPVMMGERNDAAAAAQAQGVQLRIGGLPPWMLSHLNA-----
 20912 -----ATPSTSSPTPVTA DPPIPTTNNSQSQPRGSGES-----EAQPSPAQAAGNSKLPWPWMLRTSHT-----
 19788 GS-----STVLADQPHHHQGLLHPHPDQGDHSLQIGYH-----HPH-AHHHQAYMDHLSNEAADWVAHHPNEHIPSGWI-----
 20770 G-----HASEANQEFLLHHAICDP-----SLHIGY-----QAYMDHLNQ-----
 20231 QP-----EVQQ-PLHGGNGFFHPLDAAAGEPTLQIGYP-----AEHHEAMNSACMNTYMPWPWP-----
 21116 QP-----EVQQ-PLHGGNGFFHPLDAAAGEPTLQIGYP-----AEHHEAMNSACMNTYMPWPWP-----
 20778 QSP-----HAVQQVPPHGGNGFFHSLAAAEPTLQIGFT-----PEQ---MNNSCVTAFMPTWLP-----
 20233 -----AVVENG-AAVYVQPPPHSAAMDSEPTLQIGYP-----HQFVPAEANTIQRSTAPAGAE-----NNFMLGWVL-----
 20914 -----TVVSGGRVLNAQPPPD---IDCEPTLQIGY-----YQFVRPEAANPRSNNGGGDQN-----NNFVMGWPL-----
 20698 -----AWPRDVPMTSSTAGAADAMDVETDLYIGLP-----GTERSSNRSETG-----
 20668 -----QAAAAAQQQQONPFVAQAALDMKCFPLNLFEAAAQVQAVAAQRQOIIPTELNLGYHHHIAIPGATAADAPPPHF-----
 20700 -----TSEYDHMVNNPY-----DSRNFLOVNIMQ---QPQYAHQLQ---PTTLQLGQQPAFN-----
 29949 -----RGATANESSSTPY-----SFRIIQANMPPPSLELSQSQQREGECSKTAAPGLGLHP-----
 20278 -----GAGAGAAAD-----MFAFRVVPSPNHLHGMAYGGN---HDLRLG-----
 20837 -----SSESVM TALHSGSSSQSDNDGSDVSLKGLPCGAWK-----
 20847 -----SSESVTNASYP--RPPPDNDYSSDTSCLKGLHS-----

FIGURE 3B

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Cons. -----MGRGRVELKRIENKINRQVTGSKRRNGLLKAYELSVLCDAEVALIIFSSRGKLYEFASS
19766 -----MGRGKVQLKRIENTINRQVTFSKRRSGLLKANEISVLCDAEVALIIFSTKGKLYKYATDS
20910 -----MGRGKVQLKRIENKINRQVTFSKRRSKLLKKANEISVLCDAEVALIIFSTKGKLYEYATDS
20232 -----MGRGKVQLKRIENKINRQVTFSKRRSGLLKANEISVLCDAEVALIIFSTKGKLYEYATDS
20842 -----MGRGKVQLKRIENKINRQVTFSKRRNGLLKKAHEISVLCDAEVAIIFSPKGLYEYATDS
20912 -----MGRGPVQLRRRIENKINRQVTFSKRRNGLLKKAHEISVLCDAEVALIIVFSTKGKLYEYATDS
19788 -----MGRGKVELKRIENKISRQVTFAKRRNGLLKAYELSVLLCDAEVALIIFSGRGLFEFSSSS
20770 -----MGRGKVELKRIENKISRQVTFAKRRNGLLKAYELSVLCDAEVALIIFSTRGRLFEFSTSS
20231 -----MGRGRVELKRIENKINRQVTFAKRRNGLLKAYELSVLCDAEVALIIFSNRGKLYEFCSTQ
21116 LVGGSWRSIGMGRGRVELKRIENKINRKVTFAKRRNGLLKAYELSVLCDAEVALIIFSNRGKLYEFCSTQ
20778 -----MGRGRVELKRIENKINRQVTFAKRRNGLLKAYELSVLCDAEVALIIFSNRGKLYEFCSGQ
20233 -----MGRGRVELKRIENKINRQVTFSKRRNGLLKAYELSVLCDAEVALIIFSSRGKLYEFGSAG
20914 -----MGRGRVELKRIENKINRQVTFSKRRNGLLKAYELSVLCDAEVALIIFSSRGKLYEFGSAG
20698 MV-----RGRTTELKRIENTSRQVTFSKRRNGLLKAFELSVLCDAEVALIIVFSPRGRLYEFASAP
20668 -----MGRGRIEIKRIENTSRQVTFCKRRNGLLKAYELSVLCDAEVALIIVFSSRGRLYEYSNNN
20700 -----MGRGKIEIKRIENTNRQVTFCKRRNGLLKAYELSVLCDAEVALIIVFSSRGRLYEYANN-
29949 -----MGRGKIVIRRIDNSTSRQVTFSKRRNGLLKAKELSVLCDAEVLVFSSTGKLYEFSST-
20278 -----MGRGKIEIKRIENATNRQVTYSKRRTGIMKKARELTVLCDAQVAIIMFSSSTGKLYEFCSPST
20837 MA-----RERREIKRIESAAARQVTFSKRRRGLFKKAEELSVLCDAEVALIIVFSSSTGKLSHFASS-
20847 EGEG--RAATGKRERIAIRRIDNLAARQVTFSKRRRGLFKKAEELSVLCDAEVLVFSATGKLFQFASTS-

FIGURE 3C

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Cons. S-MTKTLERYQRYSYA-ESAVISAESETQGSWYQYELKLKAKVEALQKTQRH-----LLGEDLESLSLKELQ

19766 CMDKILERYERYSYAEK--VLI SAESDTQGNWCHEYRKLKAKVETIQKCQ-KHLMGEDLESNLNKLQ

20910 CMDKILERYERYSYAEK--VLI SAESDTQGNWCHEYRKLKAKVETIQKCQ-KHLMGEDLESNLNKLQ

20232 CMDKILERYERYSYAEK--VLI SAESDTQGNWCHEYRKLKAKVETIQKCQ-KHLMGEDLESNLNKLQ

20842 RMDKILERYERYSYAEK--ALISAESSEGNWCHEYRKLKAKIETIQKCH-KHLMGEDHESNLNKLQ

20912 SMEGILERYQRYSFDER--AVLEPNTEDQENWGDEYGIKSKLDALQKSQ-RQLLGEQLDTLTTKELQ

19788 CMYKTLERYRSCNYSN-----QDAAPENEIN-YQEYLYKLKTRVEFLQTTQ-RNLLGEDLGPLSMKELE

20770 CMYKTLERYRSCNYSN--SCEASAALETELSNYQYELKLKTRVEFLQTTQ-RNLLGEDLVPLSLKELE

20231 SMTKTLEKYQKCSYAGPETAVQNRESEQLKASRNEYLYKLKARVENLQRTQ-RNLLGEDLDSLGIKELE

21116 SMTKTLEKYQKCSYAGPETAVQNRESEQLKASRNEYLYKLKARVENLQRTQ-RNLLGEDLDSLGIKELE

20778 SMTRTLERYQKFSYGGPDTAIONKENELVQSSRNEYLYKLKARVENLQRTQ-RNLLGEDLGTGIKELE

20233 -ITKTLERYQHCCYNAQ-DSNNALS--ETQSWYHEMSKLKAKFEALQRTQ-RHLLGEDLGPLSVKELQ

20914 -INKTLEKYNSCCYNAQ-GSNSALAGGEHQSWYQEMSRLKTKLECLQRSQ-RHMLGEDLGPLSIKELQ

20698 SLQKTIIDRYKAYTKDHV---NNKTIQQDIQQVKDDTLGLAKKLEALDESR-RKILGENLEGCSIEELR

20668 NVKATIIDRYKKAHACGSTSGAPLIEVNAQQYQQESAKLRHQIQMLQNTN-KHLVGDNVSNLSLKELK

20700 SVKSTIVERYKKANSDTNSGT-VAEVNAQHY-QQESSKLQQISSLQANANSTIVGDSINTMSLRDLK

29949 NMKTVIDRYTNAKEELLGNA-----TSEIKIWQREAAASLRQQLHNLQESH-KQLMGEELSGLGVRDLQ

20278 DIKGIFDRYQQAIGTS-----LWIEQYENMORTLSHLKDINRNLRTET-RQRMGEDLDGLEFDEL

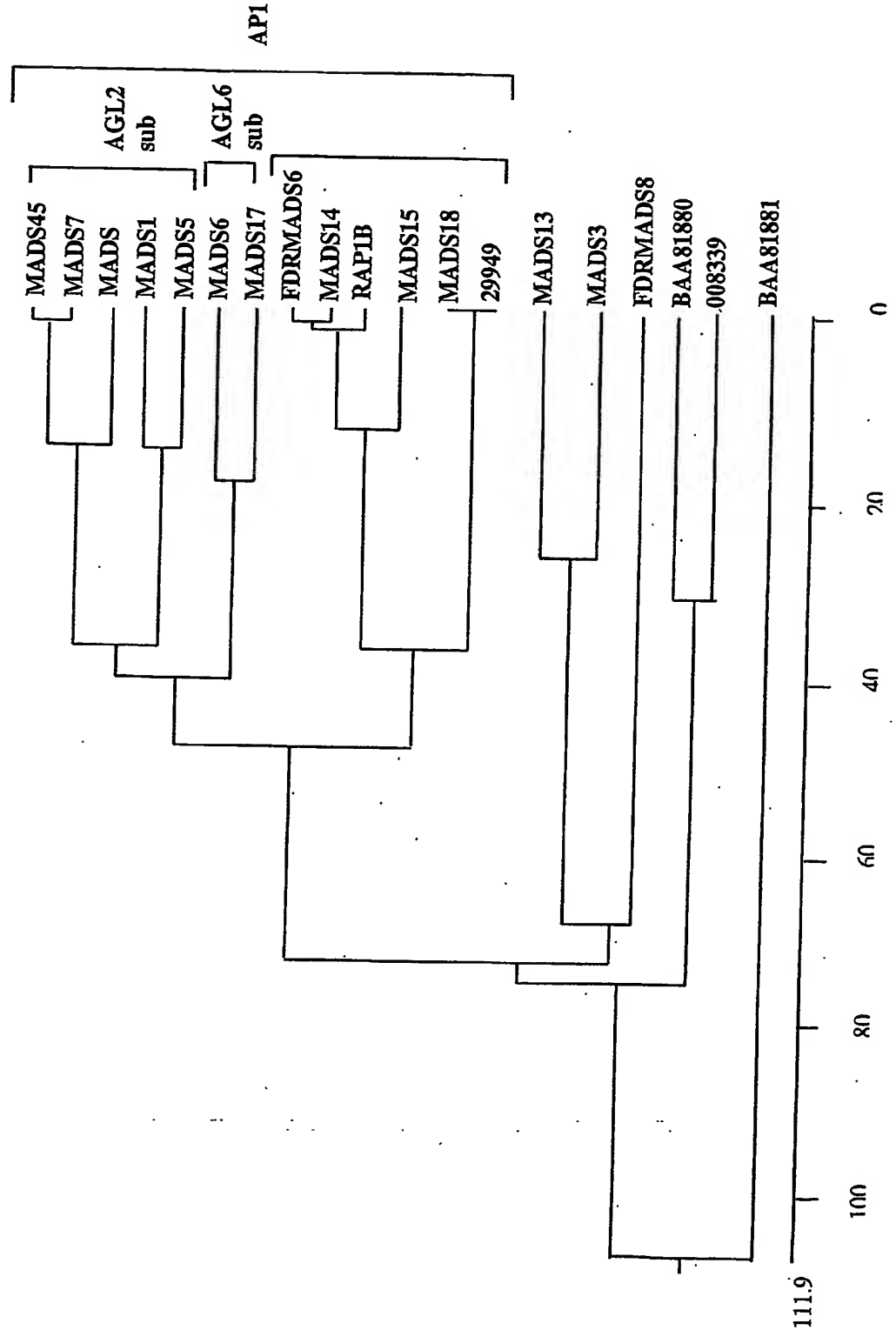
20837 -MNEIIDKYNTHSNNLG--KAEQPSLDLNLNLEHS-KYAHNLNEQLAEASLRL-RQMRGEELEGLSIDELO

20847 -MEQIIDRYNSHSHKTLQ--RAEPSQLDLOQEDSSSTCARLKEELAETSRL-RQMRGEEELHRLNVEQLQ

FIGURE 3D

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FIGURE 3E



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Fig. 4

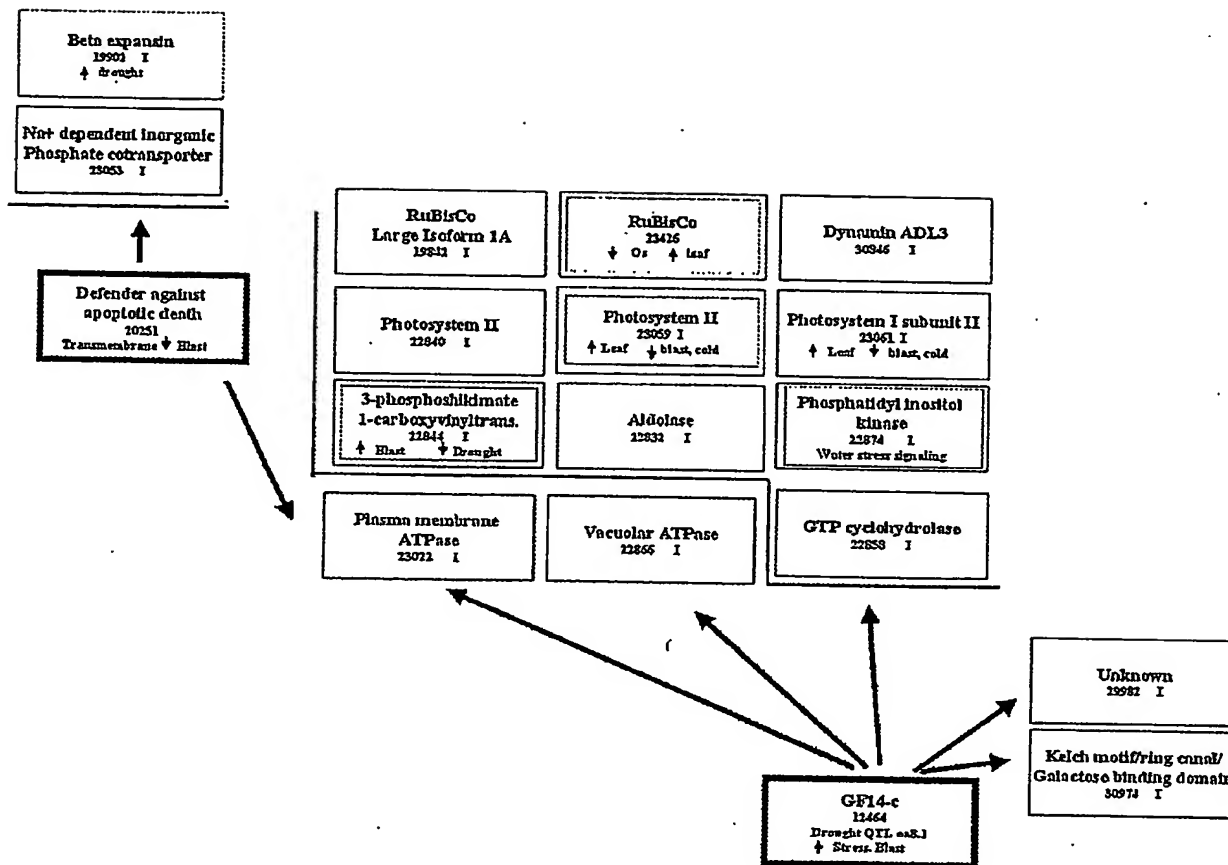
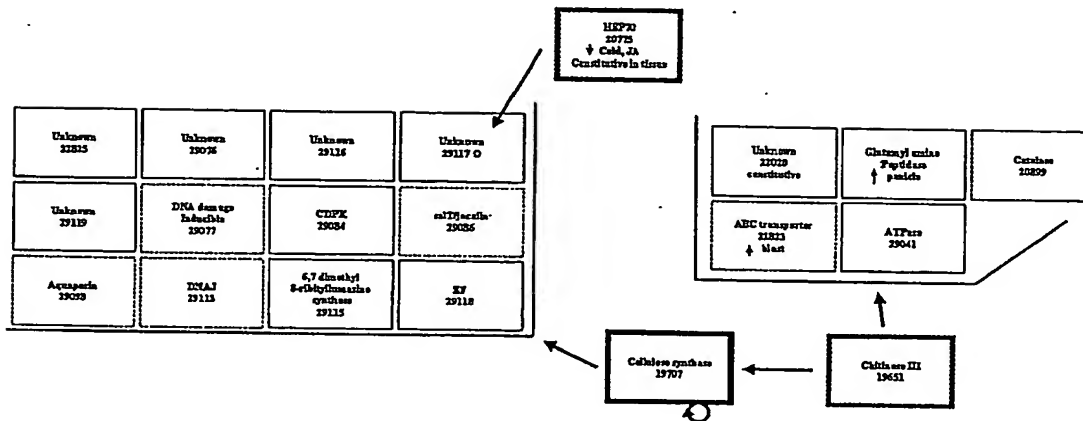


Fig. 5

CHITINASE AND CELLULOSE SYNTHASE INTERACTIONS



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Fig. 6

